
Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Reviewer Comments:

Timestamp: [year=2009; month=7; day=16; hr=13; min=14; sec=47; ms=224;]

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1.
W402
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W402
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W402
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Undefined organism found in <213> in SEQ ID (42)

Undefined organism found in <213> in SEQ ID (44)

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W402

W402

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For SEQ ID # 33 through 44, numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." For all sequences using "Unknown" or "Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank and, <223>, which states the source of the genetic material. To explain the source, if the sequence is put together from several organisms, please list those organisms. If the sequence is

made in the laboratory, please indicate that the sequence is synthesized. Please make all necessary changes.

2.										
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W213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(63)	
W213	Artificial or	Unknown	found	in	<213>	in	SEQ	ID	(64)	This
error has occur	ed more than 2	0 times,	will n	not	be dis	spla	ayed			

The warnings shown above are ok and require no response.

Validated By CRFValidator v 1.0.3

Application No: 10577003 Version No: 20

Input Set:

Output Set:

Started: 2009-06-23 16:31:45.971 Finished: 2009-06-23 16:31:49.350

72

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 379 ms

Total Warnings: 38 Total Errors: 0 No. of SeqIDs Defined: 72 Actual SegID Count:

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Input Set:

Output Set:

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Finished: 2009-06-23 16:31:49.350

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Total Warnings: 38
Total Errors: 0

No. of SeqIDs Defined: 72
Actual SeqID Count: 72

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SEQUENCE LISTING

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Ser	Gly	His 35	Ala	Ser	Ser	Thr	Pro 40	Gly	Gly	Glu	Lys	Glu 45	Thr	Ser	Ala
Thr	Glr 50	Arg	Ser	Ser	Val	Pro 55	Ser	Ser	Thr	Glu	Lys 60	Asn	Ala	Phe	Asn
Ser 65	Ser	Leu	Glu	Asp	Pro 70	Ser	Thr	Asp	Tyr	Tyr 75	Gln	Glu	Leu	Gln	Arg 80
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Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Met 115 120 125	Glu Thr	
Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn 130 135 140	Leu Thr	
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Thr Glu Lys Asn Ala Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp 50 55 60	
Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile 65 70 75 80	
Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro 85 90 95	
Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile 100 105 110	
Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala 115 120 125	
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    35 40 45
Thr Glu Lys Asn Ala Leu Ser Thr Gly Val Ser Phe Phe Leu Ser
  50
        55
                       60
Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser
65 70 75 80
Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu
      85 90 95
Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe
       100 105 110
Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
    115
            120 125
Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
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              135
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                 25
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       35
                        40
                                            45
Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln
   50
Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg
Pro Gly Ser Val Val Val Glm Leu Thr Leu Ala Phe Arg Glu Gly Thr
             85
                               90
Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tvr Lvs Thr Glu
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                            1.05
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Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp

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120

115

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cagagaagtt cagtgcccag caccgactac taccaagagc tgcagagaga catttctgaa
                                                               180
atgtttttgc agatttataa acaagggggt tttctgggcc tctccaatat taagttcagg
                                                               240
ccappatctq tqqtqqtaca attqactctq qccttccqaq aaqqtaccat caatqtccac
                                                               300
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg
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          20
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               40
Thr Glu Lys Asn Ala Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg
   50
          55
Glu Thr Phe Leu Lys Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu
               70
                                  75
65
Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
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90 95

85

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                           105
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cagagaagtt cagtgcccag ctctactgag aagaatgcta tcccagcacc gactactacc
                                                              180
aagagetgea gagagacatt tetgaaatgg ceaggatetg tggtggtaca attgactetg
                                                              240
gccttccgag aaggtaccat caatgtccac gacatggaga cacagttcaa tcagtataaa
                                                              300
acggaagcag cetetegata taacetgaeg ateteagaeg teagegtgag tgatgtgeea
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ttteetttet etgeceagte tggggetggg
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Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tvr Lvs Gln Glv Glv
          20
                           25
                                              30
Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val
      35 40 45
Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val
  50
                   55
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Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn
65
                70
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ttcaggccag gatctgtggt ggtacaattg actctggcct tccgagaagg taccatcaat
                                                            180
gtccacgaca tggagacaca gttcaatcag tataaaacgg aagcagcctc tcgatataac
ctgacgatct cagacgtcag cgtgagtgat gtgccatttc ctttctctgc ccagtctggg
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gct ggg
                                                            306
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                          25
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
      35 40 45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
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  50
                                    60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65
                70 75 80
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Pro Pro	Ala 115	His	Asp	Val	Thr	Ser 120	Ala	Pro	Asp	Asn	Lys 125	Pro	Ala	Pro
Gly Ser 130	Thr	Ala	Pro	Pro	Ala 135	His	Gly	Val	Thr	Ser 140	Ala	Pro	Asp	Thr
Arg Pro 145	Ala	Pro	Gly	Ser 150	Thr	Ala	Pro	Pro	Ala 155	His	Gly	Val	Thr	Ser 160
Ala Pro	Asp	Asn	Arg 165		Ala	Leu		Ser 170	Thr	Ala	Pro		Val 175	His
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Val His	Asn 195	Gly	Thr	Ser	Ala	Arg 200	Ala	Thr	Thr	Thr	Pro 205	Ala	Ser	Lys
Ser Thr 210					215					220				
Leu Ala 225				230					235					240
Thr Val			245					250					255	
Ser Thr		260					265					270		
Gln Phe	275					280					285			
Leu Gln 290	Arg	Asp	Ile	Ser	Glu 295	Met	Phe	Leu	GIn	300	Tyr	ГÀЗ	GIn	GIŸ

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Gly	Glu	Lys 35	Glu	Thr	Ser	Ala	Thr 40	Gln	Arg	Ser	Ser	Val 45	Pro	Ser	Ser	
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Ser 65	Pro	Gly	Ser	Gly	Ser 70	Ser	Thr	Thr	Gln	Gly 75	Gln	Asp	Val	Thr	Leu 80	
Ala	Pro	Ala	Thr	Glu 85	Pro	Ala	Ser	Gly	Ser 90	Ala	Ala	Thr	Trp	Gly 95	Gln	

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala